

5.776.760

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i i i) NUMBER OF SEQUENCES: 33

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 564 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (genomic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATTTAGCAGC	ATTCCAGATT	GGGTTCAATC	AACAAAGTAC	GAGCCATATC	ACTTATTTCA	60
AATTGOTATC	GCCAAAACCA	AGAAAGGAAC	CCCATCCTCA	AAAGTTTGTA	AOGAAGAATT	120
CTCAGTCCAA	AOCCTCAACA	AGGTCAGGGT	ACAGAGTCTC	CAAACCATTA	GCCAAAAGCT	180
ACAGGAGATC	AATGAAGAAT	CTTCAATCAA	AGTAAACTAC	TGTTCCAGCA	CATGCATCAT	240
GOTCAATAAG	TTTCAGAAAA	AGACATCCAC	CGAAAGACTTA	AAATTAGTGG	GCACTTTTGA	300
AAGTAATCTT	GTCAACATCG	AGCAAGCTGG	TTGTGGGGAC	CAGACAAAAA	AGGAATGGTG	360
CAGAATTGTT	AGGCOCACCT	ACCAAAAAGCA	TCTTTGCCCT	TATTGCAAAA	GATAAAGCAG	420

002020-070250

-continued

ATTCCTCTAG	TACAAAGTGGG	GAACAAAAATA	ACGTGGAAAA	GAGCTGTCCT	GACAGCCAC	480
TCACTAATGC	GTATGACGAA	CGCAGTGACG	ACCACAAAAA	AATTTTCCT	CTATATAAGA	540
AGGCATTICA	TTCCATTIG	AAGG				564

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATCATCAGAT ACTAACCAAT ATTCTC

27

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1692 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

NCAITGGACGT	CTGATCGAAA	TCGTCGTTAC	CGCAGCAAGG	TAAAGCACGC	CGAATTTTAT	60
CACCTACCGC	GAAACGGTGG	CTAGGCAAGC	AGAGACTGTC	GGCTCCGCGG	GAGCATCCTA	120
TGTCTGAGAA	CCACAAAAAA	GTAGGCATCG	CTGGAGCCGG	AATCGTCGGC	GTATGCACGG	180
CGCTGATGCT	TCAGCGCCGC	GGATTCAAAA	TCACCTTGAT	TGACCCGAAC	CCTCCTGGCG	240
AAAGTGCATC	GTTTGGGAAT	GCCGGATGCT	TCAACGGCTC	ATCCGTCGTC	CCTATGTCCA	300
TGCCGGGAAA	CTTGACGAGC	GTGCCGAAGT	GGCTCCTTGA	CCCGATGGGG	CCGTTGTCAA	360
TCCGGTTCAG	CTATTTTCCA	ACCATCATGC	CCTGGTTGAT	TCGCTTTCTG	TTAGCCGGAA	420
GACCAAAACA	GGTGAAAGGA	CAAGCGAAAA	CACCTCCGCA	TCTCATCAA	TCCACGGTGC	480
CTCTGATCAA	GTGATTTGGC	GAGGAAGGCT	ATGCGAGCCA	TCTGATCCGC	CATGAAGGTC	540
ATCTGACCGT	ATATCGTGGG	GAAAGCAGACT	TCGCCAAGGA	CCGCGGAAGT	TGGGAAGTGC	600
GGCGTCTCAA	CGGTGTTTCG	ACGCAAGATC	TCAGCGCCGA	TGCGTTGCGG	GATTTGATC	660
CGAACTTGTG	GCAATGCCTT	ACCAAGGGCA	TTCTTATAGA	AGAGAACGGT	CACACGATTA	720
ATCCGCAAGG	GCTCGTGACC	CTCTTGTTTC	GGCGTTTTAT	CGCGAACGGT	GGCGAATTTC	780
TATCTGCGCG	TGTCATCGGC	TTTGAGACTG	AAAGTAAAGG	GCTTAAAGGC	ATTACAACCA	840
CGAACGGCGT	TCTGGCCGTT	GATGCAAGCG	TTGTGCGAAG	CGGCGCACAC	TCGAAATCAC	900
TTGCTAATTC	GCTAGGCGAT	GACATCCCGC	TCGATACCGA	ACGTGGATAT	CATATCGTCA	960
TCGCGAATCC	GGAAGCCGCT	CCACGCATTC	CGACGACCGA	TGCGTCAGGA	AAATTCATCG	1020
CGACACCTAT	GGAATAGGGG	CTTCGCGTGG	CGGGTACGGT	TGAGTTGCGT	GGGCTCACAG	1080
CCGCTCCTAA	CTGGAAACGT	GCGCATGTGC	TCTATACGCA	CGCTCGAAAA	CTTCTTCCAG	1140
CCCTCGCGCC	TGCGAGTTCT	GAAAGAACGAT	ATTCCAAATG	GATGGGGTTC	CGGCCGAACA	1200
TCCCGGATTC	GCTCCCCGTG	ATTGGCCGGG	CAACCCGGAC	ACCCGACGTA	ATCTATGCTT	1260
TCGGCCATGG	TCATCTCGGC	ATGACAGGGG	CGCCGATGAC	CGCAACGCTC	GTCTCAGAGC	1320
TCCTCGCAGG	CGAAAAAGAC	TCAATCGACA	TTTCGCCCTT	CGCACCAAAAC	CGCTTTGGTA	1380

002020-10421950

-continued

TTGGCAAATC CAAGCAAACG GGTCCGGCAA GTTAAGTACT TACGCGOTCG TGAGTACAGC	1440
GCAGAGCCGG TGTCAAGATC AATCTGCACC TCGCAATCAC CTCGGAGACG CGAAATGGCG	1500
CAAAATAGAAC ACATATTAAC GAGTCACGCC CCGAAGCCTT TGGGTCACCTA CAGTCAGGCG	1560
GCCCGAGCGG GTGGAATTCAT TCATGTTTCC GGTACAGCTTC CGATCAAACC AGAAGGCCAG	1620
TCGGAGCAAT CTGACGATCT CGTCGATAAC CAGGCCAGTC TCGTTCTCCG GAATTTGCTG	1680
GCCGTACTCG AG	1692

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1293 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (genomic)

(i x) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1293

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATG TCT GAG AAC CAC AAA AAA GTA GGC ATC GCT GGA OCC GGA ATC GTC	48
Met Ser Glu Asn His Lys Lys Val Gly Ile Ala Gly Ala Gly Ile Val	
1 5 10 15	
GGC GTA TGC ACG GCG CTG ATG CTT CAG CGC CGC GGA TTC AAA GTC ACC	96
Gly Val Cys Thr Ala Leu Met Leu Glu Arg Arg Gly Phe Lys Val Thr	
20 25 30	
TTG ATT GAC CCG AAC CCT CCT GGC GAA GGT GCA TCG TTT GGG AAT OCC	144
Leu Ile Asp Pro Asn Pro Pro Gly Glu Gly Ala Ser Phe Gly Asn Ala	
35 40 45	
GGA TGC TTC AAC GGC TCA TCC GTC GTC CCT ATG TCC ATG CCG GGA AAC	192
Gly Cys Phe Asn Gly Ser Ser Val Val Pro Met Ser Met Pro Gly Asn	
50 55 60	
TTG ACG AGC GTG CCG AAG TGG CTC CTT GAC CCG ATG GGC COT TOT CAA	240
Leu Thr Ser Val Pro Lys Trp Leu Leu Asp Pro Met Gly Arg Cys Glu	
65 70 75 80	
TCC GGT TCA GCT ATT TCC AAC CAT CAT OCC TGG TTG ATT CGC TTT CTG	288
Ser Gly Ser Ala Ile Ser Asn His His Ala Trp Leu Ile Arg Phe Leu	
85 90 95	
TTA GCC GGA AGA CCA AAC AAG GTG AAG GAG CAG GCG AAA GCA CTC CGC	336
Leu Ala Gly Arg Pro Asn Lys Val Lys Glu Glu Ala Lys Ala Leu Arg	
100 105 110	
AAT CTC ATC AAG TCC ACG GTG CCT CTG ATC AAG TCA TTG GCG GAG GAG	384
Asn Leu Ile Lys Ser Thr Val Pro Leu Ile Lys Ser Leu Ala Glu Glu	
115 120 125	
GCT GAT GCG AGC CAT CTG ATC CGC CAT GAA GGT CAT CTG ACC GTA TAT	432
Ala Asp Ala Ser His Leu Ile Arg His Glu Gly His Leu Thr Val Tyr	
130 135 140	
COT GGA GAA GCA GAC TTC GCC AAG GAC CGC GGA GGT TGG GAA CTG CGG	480
Arg Gly Glu Ala Asp Phe Ala Lys Asp Arg Gly Gly Trp Glu Leu Arg	
145 150 155 160	
COT CTC AAC GGT GTT CCG ACG CAG ATC CTC AGC GCC GAT GCG TTT CGG	528
Arg Leu Asn Gly Val Arg Thr Glu Ile Leu Ser Ala Asp Ala Leu Arg	
165 170 175	
GAT TTC GAT CCG AAC TTT TCG CAT GCG TTT ACC AAG GGC ATT CTT ATA	576
Asp Phe Asp Pro Asn Leu Ser His Ala Phe Thr Lys Gly Ile Leu Ile	
180 185 190	
GAA GAG AAC GGT CAC ACG ATT AAT CCG CAA GGG CTC GTG ACC CTC TTG	624
Glu Glu Asn Gly His Thr Ile Asn Pro Glu Gly Leu Val Thr Leu Leu	

002204040700

-continued

195					200					205						
TTT	CGG	CGT	TTT	ATC	GCG	AAC	GGT	GGC	GAA	TTC	GTA	TCT	GCG	CGT	GTC	672
Phe	Arg	Arg	Phe	Ile	Ala	Asn	Gly	Gly	Glu	Phe	Val	Ser	Ala	Arg	Val	
	210					215					220					
ATC	GGC	TTT	GAG	ACT	GAA	GGT	AGG	GCG	CTT	AAA	GGC	ATT	ACA	ACC	ACG	720
Ile	Gly	Phe	Glu	Thr	Glu	Gly	Arg	Ala	Leu	Lys	Gly	Ile	Thr	Thr	Thr	
225					230					235					240	
AAC	GGC	GTT	CTG	GCC	GTT	GAT	GCA	GCG	GTT	GTC	GCA	GCC	GGC	GCA	CAC	768
Asn	Gly	Val	Leu	Ala	Val	Asp	Ala	Ala	Val	Val	Ala	Ala	Gly	Ala	His	
				245					250					255		
TCG	AAA	TCA	CTT	GCT	AAT	TCG	CTA	GGC	GAT	GAC	ATC	CCG	CTC	GAT	ACC	816
Ser	Lys	Ser	Leu	Ala	Asn	Ser	Leu	Gly	Asp	Asp	Ile	Pro	Leu	Asp	Thr	
			260					265					270			
GAA	CGT	GGA	TAT	CAT	ATC	GTC	ATC	GCG	AAT	CCG	GAA	GCC	GCT	CCA	CGC	864
Glu	Arg	Gly	Tyr	His	Ile	Val	Ile	Ala	Asn	Pro	Glu	Ala	Ala	Pro	Arg	
		275					280					285				
ATT	CCG	ACG	ACC	GAT	GCG	TCA	GGA	AAA	TTC	ATC	GCG	ACA	CCT	ATG	GAA	912
Ile	Pro	Thr	Thr	Asp	Ala	Ser	Gly	Lys	Phe	Ile	Ala	Thr	Pro	Met	Glu	
290						295					300					
ATG	GGG	CTT	CGC	GTG	GCG	GGT	ACG	GTT	GAG	TTC	GCT	GGG	CTC	ACA	GCC	960
Met	Gly	Leu	Arg	Val	Ala	Gly	Thr	Val	Glu	Phe	Ala	Gly	Leu	Thr	Ala	
305					310					315					320	
GCT	CCT	AAC	TGG	AAA	CGT	GCG	CAT	GTG	CTC	TAT	ACG	CAC	GCT	CGA	AAA	1008
Ala	Pro	Asn	Trp	Lys	Arg	Ala	His	Val	Leu	Tyr	Thr	His	Ala	Arg	Lys	
				325				330					335			
CTT	CTT	CCA	GCC	CTC	GCG	CCT	GCG	AGT	TCT	GAA	GAA	CGA	TAT	TCC	AAA	1056
Leu	Leu	Pro	Ala	Leu	Ala	Pro	Ala	Ser	Ser	Glu	Glu	Arg	Tyr	Ser	Lys	
			340					345					350			
TGG	ATG	GGG	TTC	CGG	CCG	AOC	ATC	CCG	GAT	TCG	CTC	CCC	GTG	ATT	GGC	1104
Trp	Met	Gly	Phe	Arg	Pro	Ser	Ile	Pro	Asp	Ser	Leu	Pro	Val	Ile	Gly	
		355					360					365				
CGG	GCA	ACC	CGG	ACA	CCC	GAC	GTA	ATC	TAT	GCT	TTC	GGC	CAT	GGT	CAT	1152
Arg	Ala	Thr	Arg	Thr	Pro	Asp	Val	Ile	Tyr	Ala	Phe	Gly	His	Gly	His	
	370					375					380					
CTC	GGC	ATG	ACA	GGG	GCG	CCG	ATG	ACC	GCA	ACG	CTC	GTC	TCA	GAG	CTC	1200
Leu	Gly	Met	Thr	Gly	Ala	Pro	Met	Thr	Ala	Thr	Leu	Val	Ser	Glu	Leu	
385					390					395					400	
CTC	GCA	GGC	GAA	AAO	ACC	TCA	ATC	GAC	ATT	TCG	CCC	TTC	GCA	CCA	AAC	1248
Leu	Ala	Gly	Glu	Lys	Thr	Ser	Ile	Asp	Ile	Ser	Pro	Phe	Ala	Pro	Asn	
				405					410					415		
CGC	TTT	GGT	ATT	GGC	AAA	TCC	AAG	CAA	ACG	GGT	CCG	GCA	AGT	TAA		1293
Arg	Phe	Gly	Ile	Gly	Lys	Ser	Lys	Glu	Thr	Gly	Pro	Ala	Ser			
			420					425					430			

(2) INFORMATION FOR SBQ ID NO-5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 430 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SBQ ID NO-5:

Met Ser Glu Asn His Lys Lys Val Gly Ile Ala Gly Ala Gly Ile Val
 1 5 10 15

Gly Val Cys Thr Ala Leu Met Leu Glu Arg Arg Gly Phe Lys Val Thr
 20 25 30

Leu Ile Asp Pro Asn Pro Pro Gly Glu Gly Ala Ser Phe Gly Asn Ala
 35 40 45

Gly Cys Phe Asn Gly Ser Ser Val Val Pro Met Ser Met Pro Gly Asn

5,776,760

51

52

-continued

50					55					60					
Leu 65	Thr	Ser	Val	Pro	Lys 70	Trp	Leu	Leu	Asp	Pro 75	Met	Gly	Arg	Cys	Gln 80
Ser	Gly	Ser	Ala	Ile 85	Ser	Asn	His	His	Ala 90	Trp	Leu	Ile	Arg	Phe 95	Leu
Leu	Ala	Gly	Arg 100	Pro	Asn	Lys	Val	Lys 105	Glu	Gln	Ala	Lys	Ala 110	Leu	Arg
Asn	Leu	Ile 115	Lys	Ser	Thr	Val	Pro 120	Leu	Ile	Lys	Ser	Leu 125	Ala	Glu	Glu
Ala	Asp 130	Ala	Ser	His	Leu	Ile 135	Arg	His	Glu	Gly	His 140	Leu	Thr	Val	Tyr
Arg 145	Gly	Glu	Ala	Asp	Phe 150	Ala	Lys	Asp	Arg	Gly 155	Gly	Trp	Glu	Leu	Arg 160
Arg	Leu	Asn	Gly	Val 165	Arg	Thr	Gln	Ile	Leu 170	Ser	Ala	Asp	Ala	Leu 175	Arg
Asp	Phe	Asp	Pro 180	Asn	Leu	Ser	His	Ala 185	Phe	Thr	Lys	Gly	Ile 190	Leu	Ile
Glu	Glu	Asn 195	Gly	His	Thr	Ile	Asn 200	Pro	Gln	Gly	Leu	Val 205	Thr	Leu	Leu
Phe	Arg 210	Arg	Phe	Ile	Ala	Asn 215	Gly	Gly	Glu	Phe	Val 220	Ser	Ala	Arg	Val
Ile 225	Gly	Phe	Glu	Thr	Glu 230	Gly	Arg	Ala	Leu	Lys 235	Gly	Ile	Thr	Thr	Thr 240
Asn	Gly	Val	Leu	Ala 245	Val	Asp	Ala	Ala	Val 250	Val	Ala	Ala	Gly	Ala 255	His
Ser	Lys	Ser	Leu 260	Ala	Asn	Ser	Leu	Gly 265	Asp	Asp	Ile	Pro	Leu 270	Asp	Thr
Glu	Arg	Gly 275	Tyr	His	Ile	Val	Ile 280	Ala	Asn	Pro	Glu	Ala 285	Ala	Pro	Arg
Ile	Pro 290	Thr	Thr	Asp	Ala	Ser 295	Gly	Lys	Phe	Ile	Ala 300	Thr	Pro	Met	Glu
Met 305	Gly	Leu	Arg	Val	Ala 310	Gly	Thr	Val	Glu	Phe 315	Ala	Gly	Leu	Thr	Ala 320
Ala	Pro	Asn	Trp	Lys 325	Arg	Ala	His	Val	Leu 330	Tyr	Thr	His	Ala	Arg 335	Lys
Leu	Leu	Pro	Ala 340	Leu	Ala	Pro	Ala	Ser 345	Ser	Glu	Glu	Arg	Tyr 350	Ser	Lys
Trp	Met	Gly 355	Phe	Arg	Pro	Ser	Ile 360	Pro	Asp	Ser	Leu	Pro 365	Val	Ile	Gly
Arg	Ala 370	Thr	Arg	Thr	Pro	Asp 375	Val	Ile	Tyr	Ala	Phe 380	Gly	His	Gly	His
Leu 385	Gly	Met	Thr	Gly	Ala 390	Pro	Met	Thr	Ala	Thr 395	Leu	Val	Ser	Glu	Leu 400
Leu	Ala	Gly	Glu	Lys 405	Thr	Ser	Ile	Asp	Ile 410	Ser	Pro	Phe	Ala	Pro 415	Asn
Arg	Phe	Gly 420	Ile	Gly	Lys	Ser	Lys	Gln 425	Thr	Gly	Pro	Ala	Ser 430		

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1296 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: double

(D) TOPOLOGY: linear

002020 "4042960

-continued

(i i) MOLECULE TYPE: DNA (recombinant)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```

ATGGCTGAGA ACCACAAAAA AGTAGGCATC GCTGGAAGCCG GAATCGTCGG CGTATGCACG      60
GCCTGATGTC TTCAAGCGCCG CGGATTCAAA GTCACCTTGA TTGACCCGAA CCCTCCTGCG      120
GAAGGTGCAT CGTTTGGGAA TGCCGGATGC TTCAACGGCT CATCCGTCGT CCCTATGTCC      180
ATGCCGGGAA ACTTGACGAG CGTGCCGAAAG TGGCTCCTTG ACCCGATGGG GCCGTGTGCA      240
ATCCGGTTCA GCTATTTTCC AACCATCATG CCCTGGTTGA TTCGCTTTCT GTTAAGCCGA      300
AGACCAAAACA AGGTGAAGGA GCAAGCGAAA GCACTCCGCA ATCTCATCAA GTCCACGGTG      360
CCTCTGATCA AGTCATTGGC GGAAGGAAGCT GATGCGAAGCC ATCTGATCCG CCATGAAGGT      420
CATCTGACCG TATATCGTGG AGAAGCAGAC TTCGCCAAGG ACCCGGGAAG TTGGGAACTG      480
CGGCGTCTCA ACGGTGTTCG CACGCAAGATC CTCAGCGCCG ATGCGTTGCG GGATTTCGAT      540
CCGAACCTGT CGCATGCGTT TACCAAAGGC ATTCTTATAG AAGAGAACGG TCACACGATT      600
AATCCGCAAG GGCTCGTGAC CCTCTTGT TT CGGCGTTTTA TCGCGAACGG TGGCGAATTT      660
GTATCTGCGC GTGTATCGG CTTTGAAGACT GAAAGTAGGG CGCTTAAAGG CATTACAACC      720
ACGAACGGCG TTCTGGCCGT TGATGCAAGC GTTGTGCGAG CCGGCGCACA CTCGAAATCA      780
CTTGCTAATT CGCTAGGCGA TGACATCCCG CTCGATACCG AACGTGGATA TCATATCGTC      840
ATCGCGAATC CGGAAGCCGC TCCACGCAAT CCGACGACCG ATGCGTCAGG AAAATTTCATC      900
CGGACACCTA TGGAAATGGG GCTTCGCGTG GCGGGTACGG TTGAGTTGCG TGGGCTCACA      960
GCCGCTCCTA ACTGGAAGCG TGCGCATGTG CTCTATACGC ACGCTCGAAA ACTTCTTCCA     1020
GCCCTCGCGC CTGCGAGTTC TGAAGAACGA TATTCCAAAT GGATGGGGTT CCGGCCGAGC     1080
ATCCCGGATT CGCTCCCCGT GATTGGCCGG GCAACCCGGA CACCCGACGT AATCTATGCT     1140
TTCGGCCACG GTCATCTCGG CATGACAGGG GCGCCGATGA CCGCAACGCT CGTCTCAGAG     1200
CTCCTCGCAG GCGAAAAGAC CTCAATCGAC ATTTCGCCCT TCGCACCAAA CCGCTTTGGT     1260
ATTGGCAAAAT CCAAAGCAAAAC GGGTCCGACA AGTTAA                               1296

```

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1296 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (recombinant)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```

ATGGCTGAGA ACCACAAAAA AGTAGGCATC GCTGGAAGCTG GAATCGTTGG TGTATGCACT      60
GCTTGTGATG TTCAACGTCG TGGATTCAAA GTCACCTTGA TTGACCCGAA CCCTCCTGCG      120
GAAGGTGCAT CGTTTGGGAA TGCCGGATGC TTCAACGGCT CATCCGTCGT CCCTATGTCC      180
ATGCCGGGAA ACTTGACGAG CGTGCCGAAAG TGGCTCCTTG ACCCGATGGG GCCGTGTGCA      240
ATCCGGTTCA GCTATTTTCC AACCATCATG CCCTGGTTGA TTCGCTTTCT GTTAAGCCGA      300
AGACCAAAACA AGGTGAAGGA GCAAGCGAAA GCACTCCGCA ATCTCATCAA GTCCACGGTG      360
CCTCTGATCA AGTCATTGGC GGAAGGAAGCT GATGCGAAGCC ATCTGATCCG CCATGAAGGT      420
CATCTGACCG TATATCGTGG AGAAGCAGAC TTCGCCAAGG ACCCGGGAAG TTGGGAACTG      480
CGGCGTCTCA ACGGTGTTCG CACGCAAGATC CTCTCTGCTG ATGCTTTGCG TGATTTCGAT      540
CCTAACCTGT CGCATGCTTT TACCAAAGGC ATTCTTATAG AAGAGAACGG TCACACGATT      600

```

-continued

AATCCGCAAG	GGCTCGTGAC	CCTCTTGTTT	CGGCGTTTTA	TCGCGAACGG	TGCGGAATTT	660
GTATCTGCOC	GTGTATCGG	TTTTGAGACT	GAAAGTCGTG	CTCTCAAAGG	CATTACAACC	720
ACTAACGGTG	TTCCTGGCTGT	TGATGCAGCT	GTTGTTGCAO	CTGGTGCACA	CTCTAAATCA	780
CTTGCTAATT	CGCTAGGCGA	TGACATCCCG	CTCGATACCG	AACGTGGATA	TCATATCGTC	840
ATCGCGAATC	CGGAAGCCGC	TCCACGCATT	CCGACGACCG	ATGCCTCAOG	AAAATTCATC	900
GCGACACCTA	TGGAAATGGG	TCITCGTGTT	GCTGGTACTG	TIGAGTTTGC	TGGTCTCACA	960
GCTGCTCCTA	ACTGGAAACG	TGCGCATGTG	CTCTATACGC	ACGCTCGAAA	ACTTCTTCCA	1020
GCCCTCGCOC	CTGCGAGTTC	TGAAGAACGA	TATTCCAAAT	GGATGGGTTT	TCCTCTAGC	1080
ATTCTGATT	CTCTTCCAGT	GATTGGTCGT	GCAACTCGTA	CACCCGACGT	AATCTATGCT	1140
TTTGGTCACG	GTCTATCTCG	TATGACAGGT	GCTCCAATGA	CTGCAACTCT	CGTCTCAGAG	1200
CTCCTCGCAG	GCGAAAAGAC	CTCAATCGAC	ATTTGCCCT	TCGCACCAAA	CCGCTTTGGT	1260
ATTGGCAAAT	CCAAGCAAAC	GGGTCCGGCA	AGTTAA			1296

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1296 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (synthetic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATGGCTGAGA	ACCACAAGAA	GGTTGGTATC	GCTGGAGCTG	GAATCGTTGG	TGTTTGCACT	60
GCTTTGATGC	TTCAACGTCT	TGGAATCAAG	GTTACCTTGA	TGATCCAAA	CCCACCAAGT	120
GAAAGTGCTT	CTTTCGGTAA	CGCTGGTTGC	TTCAACGGTT	CCTCCGTTGT	TCCAATGTCC	180
ATGCCAGGAA	ACTTGACTAG	CGTTCCAAAG	TGGCTTCTTG	ACCCAATGGG	TCCATTGTCC	240
ATCCGTTTCA	GCTACTTTCC	AACCATCATG	CCTTGGTTGA	TTGGTTTCTT	GCTTGGTGGG	300
AGACCAAAACA	AAGTGAAAGG	GCAAGCTAAG	GCACTCCGTA	ACCTCATCAA	GTCCACTGTG	360
CCTTTGAICA	AGTCCTTGGC	TGAGGAGGCT	GATGCTAGCC	ACCTTATCCG	TCACGAAAGT	420
CACCTTACCG	TGTACCGTGG	AGAAAGCAGAC	TTCGCCAAGG	ACCGTGGAGG	TTGGGAACIT	480
CGTCGTCTCA	ACGGTGTTCG	TACTCAAATC	CTCAGCGCTG	ATGCATTGCG	TGATTTGAT	540
CCTAACTTGT	CTCAGCCCTT	TACCAAGGGA	ATCCTTATCG	AAGAGAACGG	TCACACCATC	600
AACCCACAAAG	GTCTCGTGAC	TCTCTTGTTT	CGTCGTTTCA	TCGCTAACGG	TGGAGAGTTC	660
GTGTCTGCTC	GTGTTATCGG	ATTCGAGACT	GAAAGTCGTG	CTCTCAAAGG	TATCACCACC	720
ACCAACGGTG	TTCCTGCTGT	TGATGCAGCT	GTTGTTGCAO	CTGGTGCACA	CTCCAAGTCT	780
CTTGCTAACT	CCCTTGGTGA	TGACATCCCA	TTGGATACCG	AACGTGGATA	CCACATCGTG	840
ATCGCCAAACC	CAGAAAGCTGC	TCCACGTATT	CCAACTACCG	ATGCTTCTGG	AAAGTTTCATC	900
GCTACTCCTA	TGGAGATGGG	TCITCGTGTT	GCTGGAAACCG	TGAGTTTCCG	TGGTCTCACT	960
GCTGCTCCTA	ACTGGAAAGCG	TGCTCACGTT	CTCTACACTC	ACGCTCGTAA	GTTGCTTCCA	1020
GCTCTCGCTC	CTGCCAGTTC	TGAAGAACGT	TACTCCAAAT	GGATGGGTTT	CCGTCCAAAGC	1080
ATCCCAAGATT	CCCTTCCAGT	GATTGGTCGT	GCTACCCGTA	CTCCAAGACGT	TATCTACGCT	1140
TTGGTTCACG	GTACCTTCGG	TATGACTGGT	GCTCCAATGA	CCGCAACCCT	CGTTTCTGAG	1200
CTCCTCGCAG	GTGAGAAAGAC	CTCTATCGAC	ATCTCTCCAT	TCGCACCAAA	CCGTTTCCGT	1260

-continued

ATTGGTAAAGT CCAAGCAAAC TGGTCCTGCA TCCTAA

1296

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (recombinant)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AGATCTCCAC AATGGCTTCC TCTATGCTCT CTTCGGCTAC TATGGTTGCC TCTCCGGCTC 60
AGGCCACTAT GGTGCTCTCT ITCAACGGAC TTAAGTCCTC CGCTGCCTTC CCAGCCACCC 120
GCAAGGCTAA CAACGACATT ACTTCCATCA CAAGCAACGG CGGAAGAATT AACTGCATGC 180
AGGTGTGGCC TCCOATTGGA AAGAAGAAAT TTGAGACTCT CTCTTACCTT CCTGACCTTA 240
CCGATTCGGG TGGTCGCTC AACTGCATGC AGGCCATGG 279

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 318 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (recombinant)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AGATCTATCG ATAAGCTTGA TGTAAATTGGA GGAAGATCAA AATTTTCAAT CCCCATTCTT 60
CGATTGCTTC AATTGAAATT TCTCCGATGG CGCAAGTTAG CAGAATCTGC AATGGTGTGC 120
AGAACCCTATC TCTTATCTCC AATCTCTCGA AATCCAATCA ACGCAAATCT CCCTTATCGG 180
TTTCTCTGAA GACGCAGCAG CATCCACGAG CTTATCCGAT TTCCTCCTCG TGGGGATTGA 240
AQAAGAATGG GATGACOTTA ATTGGCTCTG AGCTTCGTCC TCTTAAGGTC ATGTCTTCTG 300
TTTCCACGGC GTGCATGC 318

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 119 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (genomic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:11:

NCATGGACGT CTGATCGAAA TCGTCOTTAC CGCAGCAAGG TAAGGCACGC CGAATTTTAT 60
CACCTACCGC GAAACGGTGG CTAAGCAGCG AGAGACTGTC GGCTCCCGGG GAGCATCCT 119

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 277 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (genomic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:12:

002020 "4042T950

GTACTTACGC	GGTCGTGAGT	ACAAGCGCAGA	GCCGGTGTCA	AGATCAATCT	GCACCTCGCA	60
ATCACCTCGG	AGACGCGAAA	TGGCGCAAAT	AGAACACATA	TTAACGAGTC	ACGCCCCGAA	120
GCCTTTGGGT	CACTACAGTC	AGGCGGCCCG	AQCGGGTGGA	TTCATTCATG	TTTCCGOTCA	180
GCCTCCGATC	AAACCAGAAAG	GCCAGTCGGA	GCAATCTGAC	GAICTCTGTCG	ATAACCAGGC	240
CAQTCTCGTT	CTCCGGAATT	TGCTGGCCGT	ACTCGAG			277

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAGAGACTGT CGACTCCGCG GGAGCATCAT ATG 33

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(x i) SBOUENCE DESCRIPTION: SEQ ID NO:14:

GAACGAATCC AAGCTTCTCA CGACCGCGTA AGTAC 35

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(x i) SEQUENCE DESCRIPTION: SBQ ID NO:15:

OCCGAGATGA CCGTGGCCGA AAGC 24

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:16:

000AAT0CC0 0AT0CITCAA C0GC 24

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1296 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (recombinant)

-continued

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..1296

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ATG	GCT	GAG	AAC	CAC	AAG	AAG	GTT	GGT	ATC	GCT	GGA	GCT	GGA	ATC	GTT	48
Met	Ala	Glu	Asn	His	Lys	Lys	Val	Gly	Ile	Ala	Gly	Ala	Gly	Ile	Val	
1				5				10						15		
GGT	GTT	TGC	ACT	GCT	TIG	ATG	CTT	CAA	CGT	CGT	GGA	TTC	AAG	GTT	ACC	96
Gly	Val	Cys	Thr	Ala	Leu	Met	Leu	Gln	Arg	Arg	Gly	Phe	Lys	Val	Thr	
			20					25					30			
TIG	ATT	GAT	CCA	AAC	CCA	CCA	GGT	GAA	GGT	OCC	TCT	TTC	GGT	AAC	GCT	144
Leu	Ile	Asp	Pro	Asn	Pro	Pro	Gly	Glu	Gly	Ala	Ser	Phe	Gly	Asn	Ala	
		35					40					45				
GGT	TGC	TTC	AAC	GGT	TCC	TCC	GTT	GTT	CCA	ATG	TCC	ATG	CCA	GGA	AAC	192
Gly	Cys	Phe	Asn	Gly	Ser	Ser	Val	Val	Pro	Met	Ser	Met	Pro	Gly	Asn	
	50				55					60						
TIG	ACT	AGC	GTT	CCA	AAG	TGG	CTT	CTT	GAC	CCA	ATG	GGT	CCA	TIG	TCC	240
Leu	Thr	Ser	Val	Pro	Lys	Trp	Leu	Leu	Asp	Pro	Met	Gly	Pro	Leu	Ser	
	65				70				75						80	
ATC	CGT	TTC	GGC	TAC	TTT	CCA	ACC	ATC	ATG	CCT	TGG	TIG	ATT	CGT	TTC	288
Ile	Arg	Phe	Gly	Tyr	Phe	Pro	Thr	Ile	Met	Pro	Trp	Leu	Ile	Arg	Phe	
				85				90						95		
TIG	CTT	GCT	GGA	AGA	CCA	AAC	AAG	GTG	AAG	GAG	CAA	GCT	AAG	GCA	CTC	336
Leu	Leu	Ala	Gly	Arg	Pro	Asn	Lys	Val	Lys	Glu	Glu	Ala	Lys	Ala	Leu	
			100					105					110			
CGT	AAC	CTC	ATC	AAG	TCC	ACT	GTG	CCT	TIG	ATC	AAG	TCC	TIG	GCT	GAG	384
Arg	Asn	Leu	Ile	Lys	Ser	Thr	Val	Pro	Leu	Ile	Lys	Ser	Leu	Ala	Glu	
		115					120					125				
GAG	GCT	GAT	GCT	AGC	CAC	CTT	ATC	CGT	CAC	GAA	GGT	CAC	CTT	ACC	GTG	432
Glu	Ala	Asp	Ala	Ser	His	Leu	Ile	Arg	His	Glu	Gly	His	Leu	Thr	Val	
	130				135					140						
TAC	CGT	GGA	GAA	GCA	GAC	TTC	GCC	AAG	GAC	CGT	GGA	GGT	TGG	GAA	CTT	480
Tyr	Arg	Gly	Glu	Ala	Asp	Phe	Ala	Arg	Asp	Arg	Gly	Gly	Trp	Glu	Leu	
	145				150				155					160		
CGT	CGT	CTC	AAC	GGT	GTT	CGT	ACT	CAA	ATC	CTC	AGC	GCT	GAT	GCA	TIG	528
Arg	Arg	Leu	Asn	Gly	Val	Arg	Thr	Gln	Ile	Leu	Ser	Ala	Asp	Ala	Leu	
			165					170						175		
CGT	GAT	TTC	GAT	CCT	AAC	TIG	TCT	CAC	OCC	TTT	ACC	AAG	GGA	ATC	CTT	576
Arg	Asp	Phe	Asp	Pro	Asn	Leu	Ser	His	Ala	Phe	Thr	Lys	Gly	Ile	Leu	
			180					185					190			
ATC	GAA	GAG	AAC	GGT	CAC	ACC	ATC	AAC	CCA	CAA	GGT	CTC	GTG	ACT	CTC	624
Ile	Glu	Glu	Asn	Gly	His	Thr	Ile	Asn	Pro	Glu	Gly	Val	Val	Thr	Leu	
		195					200					205				
TIG	TTT	COT	CGT	TTC	ATC	GCT	AAC	GGT	GGA	GAG	TTC	GTG	TCT	GCT	COT	672
Leu	Phe	Arg	Arg	Phe	Ile	Ala	Asn	Gly	Gly	Glu	Phe	Val	Ser	Ala	Arg	
	210				215							220				
GTT	ATC	GGA	TTC	GAG	ACT	GAA	GGT	CGT	GCT	CTC	AAG	GGT	ATC	ACC	ACC	720
Val	Ile	Gly	Phe	Glu	Thr	Glu	Gly	Arg	Ala	Leu	Lys	Gly	Ile	Thr	Thr	
	225				230				235					240		
ACC	AAC	GGT	GTT	CTT	GCT	GTT	GAT	GCA	GCT	GTT	GTT	GCA	GCT	GGT	GCA	768
Thr	Asn	Gly	Val	Leu	Ala	Val	Asp	Ala	Ala	Val	Val	Ala	Ala	Gly	Ala	
			245					250						255		
CAC	TCC	AAG	TCT	CTT	GCT	AAC	TCC	CTT	GGT	GAT	GAC	ATC	CCA	TIG	GAT	816
His	Ser	Lys	Ser	Leu	Ala	Asn	Ser	Leu	Gly	Asp	Asp	Ile	Pro	Leu	Asp	
			260					265					270			
ACC	GAA	CGT	GGA	TAC	CAC	ATC	GTG	ATC	GCC	AAC	CCA	GAA	GCT	GCT	CCA	864
Thr	Glu	Arg	Gly	Tyr	His	Ile	Val	Ile	Ala	Asn	Pro	Glu	Ala	Ala	Pro	
		275					280					285				
CGT	ATT	CCA	ACT	ACC	GAT	GCT	TCT	GGA	AAG	TTC	ATC	GCT	ACT	CCT	ATG	912

00202404-0700

-continued

Arg	Ile	Pro	Thr	Thr	Asp	Ala	Ser	Gly	Lys	Phe	Ile	Ala	Thr	Pro	Met	
290						295					300					
GAG	ATG	GGT	CTT	CGT	GTT	GCT	GGA	ACC	GTT	GAG	TTC	GCT	GGT	CTC	ACT	960
Glu	Met	Gly	Leu	Arg	Val	Ala	Gly	Thr	Val	Glu	Phe	Ala	Gly	Leu	Thr	
305					310					315					320	
GCT	GCT	CCT	AAC	TGG	AAG	CGT	GCT	CAC	GTT	CTC	TAC	ACT	CGC	GCT	CGT	1008
Ala	Ala	Pro	Asn	Trp	Lys	Arg	Ala	His	Val	Leu	Tyr	Thr	Arg	Ala	Arg	
				325					330					335		
AAG	TTG	CTT	CCA	GCT	CTC	GCT	CCT	GCC	AGT	TCT	GAA	GAA	CGT	TAC	TCC	1056
Lys	Leu	Leu		Ala	Leu	Ala	Pro	Ala	Ser	Ser	Glu	Glu		Arg	Tyr	
			340					345					350		Ser	
AAG	TGG	ATG	GGT	TTT	CGT	CCA	AGC	ATC	CCG	GAT	TCC	CTT	CCA	GTG	ATT	1104
Lys	Trp	Met	Gly	Phe	Arg	Pro	Ser	Ile	Pro	Asp	Ser		Leu	Pro	Val	
		355					360					365			Ile	
GGT	CGT	GCT	ACC	CGT	ACT	CCA	GAC	GTT	ATC	TAC	GCT	TTC	GGT	CAC	GGT	1152
Gly	Arg	Ala	Thr	Arg	Thr	Pro	Asp	Val	Ile	Tyr	Ala	Phe	Gly	His	Gly	
	370				375						380					
CAC	CTC	GGT	ATG	ACT	GGT	GCT	CCA	ATG	ACC	GCA	ACC	CTC	GTT	TCT	GAG	1200
His	Leu	Gly	Met	Thr	Gly	Ala	Pro	Met	Thr		Ala	Thr	Leu	Val	Ser	
	385				390				395						Glu	
CTC	CTC	GCA	GGT	GAG	AAG	ACC	TCT	ATC	GAC	ATC	TCT	CCA	TTT	GCA	CCA	1248
Leu	Leu	Ala	Gly	Glu	Lys	Thr	Ser	Ile	Asp	Ile	Ser	Pro	Phe	Ala	Pro	
				405					410					415		
AAC	CGT	TTT	GCT	ATT	GGT	AAG	TCC	AAG	CAA	ACT	GGT	CCT	GCA	TCC	TAA	1296
Asn	Arg	Phe	Gly	Ile	Gly	Lys	Ser	Lys	Gln	Thr	Gly	Pro	Ala	Ser		
			420					425					430			

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 431 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

```

Met  Ala  Glu  Asn  His  Lys  Lys  Val  Gly  Ile  Ala  Gly  Ala  Gly  Ile  Val
 1          5          10          15
Gly  Val  Cys  Thr  Ala  Leu  Met  Leu  Glu  Arg  Arg  Gly  Phe  Lys  Val  Thr
          20          25          30
Leu  Ile  Asp  Pro  Asn  Pro  Pro  Gly  Glu  Gly  Ala  Ser  Phe  Gly  Asn  Ala
          35          40          45
Gly  Cys  Phe  Asn  Gly  Ser  Ser  Val  Val  Pro  Met  Ser  Met  Pro  Gly  Asn
          50          55          60
Leu  Thr  Ser  Val  Pro  Lys  Trp  Leu  Leu  Asp  Pro  Met  Gly  Pro  Leu  Ser
          65          70          75          80
Ile  Arg  Phe  Gly  Tyr  Phe  Pro  Thr  Ile  Met  Pro  Trp  Leu  Ile  Arg  Phe
          85          90          95
Leu  Leu  Ala  Gly  Arg  Pro  Asn  Lys  Val  Lys  Glu  Gln  Ala  Lys  Ala  Leu
          100          105          110
Arg  Asn  Leu  Ile  Lys  Ser  Thr  Val  Pro  Leu  Ile  Lys  Ser  Leu  Ala  Glu
          115          120          125
Glu  Ala  Asp  Ala  Ser  His  Leu  Ile  Arg  His  Glu  Gly  His  Leu  Thr  Val
          130          135          140
Tyr  Arg  Gly  Glu  Ala  Asp  Phe  Ala  Arg  Asp  Arg  Gly  Gly  Trp  Glu  Leu
          145          150          155          160
Arg  Arg  Leu  Asn  Gly  Val  Arg  Thr  Gln  Ile  Leu  Ser  Ala  Asp  Ala  Leu
          165          170          175

```

002020-1042950

-continued

Arg	Asp	Phe	Asp	Pro	Asn	Leu	Ser	His	Ala	Phe	Thr	Lys	Gly	Ile	Leu
			180					185					190		
Ile	Glu	Glu	Asn	Gly	His	Thr	Ile	Asn	Pro	Gln	Gly	Leu	Val	Thr	Leu
		195					200					205			
Leu	Phe	Arg	Arg	Phe	Ile	Ala	Asn	Gly	Gly	Glu	Phe	Val	Ser	Ala	Arg
	210					215					220				
Val	Ile	Gly	Phe	Glu	Thr	Glu	Gly	Arg	Ala	Leu	Lys	Gly	Ile	Thr	Thr
225					230					235					240
Thr	Asn	Gly	Val	Leu	Ala	Val	Asp	Ala	Ala	Val	Val	Ala	Ala	Gly	Ala
			245						250					255	
His	Ser	Lys	Ser	Leu	Ala	Asn	Ser	Leu	Gly	Asp	Asp	Ile	Pro	Leu	Asp
			260					265					270		
Thr	Glu	Arg	Gly	Tyr	His	Ile	Val	Ile	Ala	Asn	Pro	Glu	Ala	Ala	Pro
		275					280					285			
Arg	Ile	Pro	Thr	Thr	Asp	Ala	Ser	Gly	Lys	Phe	Ile	Ala	Thr	Pro	Met
	290					295					300				
Glu	Met	Gly	Leu	Arg	Val	Ala	Gly	Thr	Val	Glu	Phe	Ala	Gly	Leu	Thr
305					310					315					320
Ala	Ala	Pro	Asn	Trp	Lys	Arg	Ala	His	Val	Leu	Tyr	Thr	Arg	Ala	Arg
				325					330					335	
Lys	Leu	Leu	Pro	Ala	Leu	Ala	Pro	Ala	Ser	Ser	Glu	Glu	Arg	Tyr	Ser
			340					345					350		
Lys	Trp	Met	Gly	Phe	Arg	Pro	Ser	Ile	Pro	Asp	Ser	Leu	Pro	Val	Ile
		355					360					365			
Gly	Arg	Ala	Thr	Arg	Thr	Pro	Asp	Val	Ile	Tyr	Ala	Phe	Gly	His	Gly
	370					375					380				
His	Leu	Gly	Met	Thr	Gly	Ala	Pro	Met	Thr	Ala	Thr	Leu	Val	Ser	Glu
385					390					395					400
Leu	Leu	Ala	Gly	Glu	Lys	Thr	Ser	Ile	Asp	Ile	Ser	Pro	Phe	Ala	Pro
				405					410					415	
Asn	Arg	Phe	Gly	Ile	Gly	Lys	Ser	Lys	Gln	Thr	Gly	Pro	Ala	Ser	
			420					425					430		

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CGTTCTCTAC ACTCGTGTCTC GTAAAGTTGC

29

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (synthetic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CGTTCTCTAC ACTAAGGCTC GTAAAGTTGC

29

(2) INFORMATION FOR SEQ ID NO:21:

09612404-070700

-continued

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (synthetic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CGTTCTCTAC ACTCAAGCTC GTAAGTTGC

29

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (synthetic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CGTTCTCTAC ACTGCTGCTC GTAAGTTGC

29

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (synthetic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CTCTACACIT GGGCTCGTAA GCTTCTTCCA GC

32

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (synthetic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CTCTACACTA TGGCTCGTAA GCTTCTTCCA GC

32

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (synthetic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CTCTACACTC TGGCTCGTAA GCTTCTTCCA GC

32

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

-continued

(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (synthetic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CTCTACACTG AAGCTCGTAA GCTTCTTCCA GC

3 2

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (synthetic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CGCTGGAGCT GGAATCGTTG GTGTATGCAC TGCTTTGATG CTTCACGTC GTGGATTCAA

6 0

AG

6 2

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (synthetic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GCAGATCCTC TCTGCTGATG CTTTGCCTGA TTTCGATCCT AACTTGTCTC ATGCITTTAC

6 0

CAAGG

6 5

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (synthetic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GTCAICGGTT TTGAGACTGA AAGTCGTGCT CTCAAAAGCA T

4 1

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (synthetic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:30:

TACAACCACT AACGGTGTTC TGGCTGTTGA TGCAGCTGTT GTTCAGCTG GTGCACACTC

6 0

TAAATCACT

6 9

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 base pairs
- (B) TYPE: nucleic acid

-continued

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (synthetic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GGAAATGGGT CTTCGTGTTG CTGGTACTGT TGAGTTTGCT GGTCTCACAG CTGCTCCTAA 60
C 61

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 68 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (synthetic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TGGATGGGTT TTCGTCCTAG CATTCTGAT TCTCTTCCAG TGATTGGTCG TGCAACTCGT 60
ACACCCGA 68

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 69 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(i i) MOLECULE TYPE: DNA (synthetic)

(x i) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CGTAATCTAT GCTTTTGTC ACGGTCATCT CGGTATGACA GGTGCTCCAA TGA CTGCAAC 60
TCTCCTCTC 69

002020-7042F960